



SEQUENCE LISTING

<10> Max-Planck-Gesellschaft z.
Förd. d. Wissenschaften

<120> Plants With Modified Gene Expression

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<140> 10/030,386

<140> 2002-01-02

<150> PCT/DE00/02233

<151> 2000-07-03

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<151> 1999-07-02

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<170> PatentIn Ver. 2.1

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Arg Glu Val Asp Val Asp Leu His Ile Gly Leu Pro Gly Phe Gly Lys
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100 105 110

Ala Thr Tyr Asp Ala Gly Lys Gly Ile Glu Asn Glu Leu Ser Gly Lys
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Ser Leu Lys Gly Thr Gln Pro Arg Ala Met Leu Gly Ile Pro Cys Tyr
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Cys Cys Val Glu Gly Cys Arg Asn His Ile Asp His Pro Arg Ser Lys
195 200 205

Pro Leu Lys Asp Phe Arg Thr Leu Gln Thr His Tyr Lys Arg Lys His
210 215 220

Gly His Lys Pro Phe Ser Cys Arg Leu Cys Gly Lys Leu Leu Ala Val
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Lys Gly Asp Trp Arg Thr His Glu Lys Asn Cys Gly Lys Arg Trp Val
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Cys Val Cys Gly Ser Asp Phe Lys His Lys Arg Ser Leu Lys Asp His
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Leu Pro Pro Val Thr Pro Pro Ser Ser Phe Phe Phe Pro Gln Ser
35 40 45

Gly Asp Leu Arg Arg Pro Pro Pro Pro Thr Pro Pro Pro Ser Pro
50 55 60

Pro Leu Arg Glu Ala Leu Pro Leu Leu Ser Leu Ser Pro Ala Asn Lys
65 70 75 80

Gln Gln Asp His His Asn His Asp His Leu Ile Gln Glu Pro Pro
85 90 95

Ser Thr Ser Met Asp Val Asp Tyr Asp His His His Gln Asp Asp His
100 105 110

His Asn Leu Asp Asp Asp Asp His Asp Val Thr Val Ala Leu His Ile
115 120 125

Gly Leu Pro Ser Pro Ser Ala Gln Glu Met Ala Ser Leu Leu Met Met
130 135 140

Ser Ser Ser Ser Ser Arg Thr Thr His His His Glu Asp Met
145 150 155 160

Asn His Lys Lys Asp Leu Asp His Glu Tyr Ser His Gly Ala Val Gly
165 170 175

Gly Gly Glu Asp Asp Asp Glu Asp Ser Val Gly Gly Asp Gly Cys
180 185 190

Arg Ile Ser Arg Leu Asn Lys Gly Gln Tyr Trp Ile Pro Thr Pro Ser
195 200 205

Gln Ile Leu Ile Gly Pro Thr Gln Phe Ser Cys Pro Val Cys Phe Lys
210 215 220

Thr Phe Asn Arg Tyr Asn Asn Met Gln Met His Met Trp Gly His Gly
225 230 235 240

Ser Gln Tyr Arg Lys Gly Pro Glu Ser Leu Arg Gly Thr Gln Pro Thr
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Gly Met Leu Arg Leu Pro Cys Tyr Cys Cys Ala Pro Gly Cys Arg Asn
260 265 270

Asn Ile Asp His Pro Arg Ala Lys Pro Leu Lys Asp Phe Arg Thr Leu

275 280 285

Gln Thr His Tyr Lys Arg Lys His Gly Ile Lys Pro Phe Met Cys Arg
290 295 300

Lys Cys Gly Lys Ala Phe Ala Val Arg Gly Asp Trp Arg Thr His Glu
305 310 315 320

Lys Asn Cys Gly Lys Leu Trp Tyr Cys Ile Cys Gly Ser Asp Phe Lys
325 330 335

His Lys Arg Ser Leu Lys Asp His Ile Lys Ala Phe Gly Asn Gly His
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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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Tyr Leu Ala Phe Thr Gly Phe Leu Thr Gln Leu His His Leu Glu Ile
35 40 45

Ser Cys Leu Leu Leu Phe Phe Ser Leu Ser Ser Leu Leu Lys Leu
50 55 60

Met Ala Asp Pro Asp Cys Ile Phe Arg Asn Gly Tyr Val Asp Tyr Tyr
65 70 75 80

Asn Tyr Ser Phe Asn Tyr Ala Thr Ser Leu Ser Arg Ile Tyr Asn Ser
85 90 95

His Asp Ser Phe Phe Phe Pro Gln Ser Gly Asp Leu Arg Arg Pro
100 105 110

Pro Pro Pro Pro Thr Pro Pro Ser Pro Pro Leu Arg Glu Ala Leu
115 120 125

Pro Leu Leu Ser Leu Ser Pro Ala Asn Thr Gln Gln Asp His His His
 130 135 140

Asn His Asp His Leu Ile Gln Glu Pro Pro Ser Thr Ser Met Asp Val
 145 150 155 160

Asp Tyr Asp His His His Gln Asp Asp His His Asn Leu Asp Asp Asp
 165 170 175

Asp His Asp Val Thr Val Ala Leu His Ile Gly Leu Pro Ser Pro Ser
 180 185 190

Ala Gln Glu Met Ala Ser Leu Leu Met Met Ser Ser Ser Ser Ser Ser
 195 200 205

Ser Arg Thr Thr His His His Glu Asp Met Asn His Lys Lys Asp Leu
 210 215 220

Asp His Glu Tyr Ser His Gly Ala Val Gly Gly Glu Asp Asp Asp
 225 230 235 240

Glu Asp Ser Val Gly Gly Asp Gly Gly Cys Arg Ile Ser Arg Leu Asn
 245 250 255

Lys Gly Gln Tyr Trp Ile Pro Thr Pro Ser Gln Ile Leu Ile Gly Pro
 260 265 270

Thr Gln Phe Ser Cys Pro Val Cys Phe Lys Thr Phe Asn Arg Tyr Asn
 275 280 285

Asn Met Gln Met His Met Trp Gly His Gly Ser Gln Tyr Arg Lys Gly
 290 295 300

Pro Glu Ser Leu Arg Gly Thr Gln Pro Thr Gly Met Leu Arg Leu Pro
 305 310 315 320

Cys Tyr Cys Cys Ala Pro Gly Cys Arg Asn Asn Ile Asp His Pro Arg
 325 330 335

Ala Lys Pro Leu Lys Asp Phe Arg Thr Leu Gln Thr His Tyr Lys Arg
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Lys His Gly Ile Lys Pro Phe Met Cys Arg Lys Cys Gly Lys Ala Phe
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Ala Val Arg Gly Asp Trp Arg Thr His Glu Lys Asn Cys Gly Lys Leu
 370 375 380

Trp Tyr Cys Ile Cys Gly Ser Asp Phe Lys His Lys Arg Ser Leu Lys
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Asp His Ile Lys Ala Phe Thr Asn Gly His Gly Ala Tyr Gly Ile Asp
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Gly Ser Tyr Tyr Tyr Ser Asn Thr Thr Asn Pro Asn Tyr Ile Asn His
35 40 45

Thr His Thr Thr Ser Thr Ser Pro Asn Ser Pro Pro Leu Arg Glu Ala
50 55 60

Leu Pro Leu Leu Ser Leu Ser Pro Ile Arg His Gln Glu Gln Gln Asp
65 70 75 80

Gln His Tyr Phe Met Asp Thr His Gln Ile Ser Ser Ser Asn Phe Leu
85 90 95

Asp Asp Pro Leu Val Thr Val Asp Leu His Leu Gly Leu Pro Asn Tyr
100 105 110

Gly Val Gly Glu Ser Ile Arg Ser Asn Ile Ala Pro Asp Ala Thr Thr
115 120 125

Asp Glu Gln Asp Gln Asp His Asp Arg Gly Val Glu Val Thr Val Glu
130 135 140

Ser His Leu Asp Asp Asp Asp His His Gly Asp Leu His Arg Gly
145 150 155 160

His His Tyr Trp Ile Pro Thr Pro Ser Gln Ile Leu Ile Gly Pro Thr
165 170 175

Gln Phe Thr Cys Pro Leu Cys Phe Lys Thr Phe Asn Arg Tyr Asn Asn
180 185 190

Met Gln Asn Asn Ile Asp His Pro Arg Ala Lys Pro Leu Lys Asp Phe
195 200 205

Arg Thr Leu Gln Thr His Tyr Lys Arg Lys His Gly Ser Lys Pro Phe
210 215 220

Ala Cys Arg Met Cys Gly Lys Ala Phe Ala Val Lys Gly Asp Trp Arg
225 230 235 240

Thr His Glu Lys Asn Cys Gly Lys Leu Trp Tyr Cys Ser Cys Gly Ser
245 250 255

Asp Phe Lys His Lys Arg Ser Leu Lys Asp His Val Lys Ala Phe Gly
260 265 270

Asn Gly His Val Pro Cys Gly Ile Asp Ser Phe Gly Gly Asp His Glu
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<210> 8

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Peptide

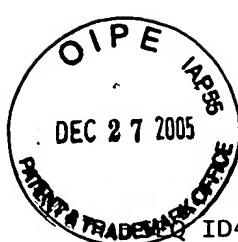
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Ser Leu Lys Gly Thr Gln Thr Val Ala Leu Leu Lys Val Pro Cys Tyr
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Cys Ala Ala Gly Cys Arg Asn Ser Val Ser His Pro Arg Ala Arg Pro
35 40 45

Leu Lys Asp Phe Arg Thr
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Note Best alignment is between forward est and forward genome, and splice sites imply forward gene

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Alignment Score: 892